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(54) Title: MULTIPLE INEXACT MATCHING

(57) Abstract: Methods and apparatus are provided for seeking, in a target sequence, an exact or inexact match to a query sequence, or each of a large number of query sequences, which could be DNA fragments for which an approximate match is sought in a genome. Initially, each query sequence is divided into segments, which are distributed between first and second segment groups. An efficient algorithm is then used to seek potential matches between a first group of segments of each query sequence and a corresponding first group of segments of each target sequence fragment.